

OM nucleic - nucleic search, using sw model

Run on: January 7, 2004, 04:41:34 ; Search time 23414 Seconds
(without alignments)

11736.139 Million cell updates/sec

Title: US-10-082-272-1

Perfect score: 6717

Sequence: 1 ggcgcgcgtcccccgcga.....taaaaaaaaaaaaaaaaaaaaaa 6717

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*			
1: gb_ba.*	2: gb_hcg.*	3: gb_in.*	4: gb_om.*
5: gb_ov.*	6: gb_pat.*	7: gb_ph.*	8: gb_pl.*
9: gb_pr.*	10: gb_ro.*	11: gb_sts.*	12: gb_sy.*
13: gb_un.*	14: gb_vi.*	15: em_ba.*	16: em_fun.*
17: em_hum.*	18: em_in.*	19: em_mu.*	20: em_om.*
21: em_or.*	22: em_ov.*	23: em_pat.*	24: em_ph.*
25: em_pl.*	26: em_ro.*	27: em_sts.*	

Result No.	Score	Query Match	Length	DB ID	Description
c 1	5237.4	78.0	177585	9	AC005826 Homo sapi
c 2	5203.8	77.5	202719	9	AC006379 Homo sapi
c 3	4812.4	71.6	188527	9	AC084357 Homo sapi
c 4	3623.4	53.9	189515	2	AC026105 Homo sapi
c 5	3350.8	49.9	150207	2	AL451067 Homo sapi
c 6	3287.6	48.9	187651	2	AC055122 Homo sapi
c 7	3275	48.8	173398	2	AC092972 Homo sapi
c 8	1554.2	23.1	3399	10	AF306667 Mus muscu
c 9	1388	20.7	187651	2	AC055122 Homo sapi
c 10	973.2	14.5	150207	2	AL451067 Homo sapi
c 11	947	14.1	1082	6	AR220868 Sequence
c 12	916.8	13.6	1323	5	AB070554 Gallus ga
c 13	831.8	12.4	1741	5	AY154394 Xenopus l
c 14	796.6	11.9	1826	10	AF260557 Mus muscu
c 15	782	11.5	2134	5	AF253325 Danio rer
c 16	769.2	11.5	2134	5	AF253325 Danio rer
c 17	765.6	11.4	246543	2	AC097034 Rattus no
c 18	734.8	10.9	982	10	MMU277486 Mus muscu
c 19	633.8	9.4	900	6	BD017880 Novel gen
c 20	633.8	9.4	900	6	BD097818 Novel gen
c 21	614.8	9.2	892	6	BD017881 Novel gen
c 22	614.8	9.2	892	6	BD097819 Novel gen
c 23	602	9.0	602	9	HS237589 Homo sapi
c 24	587.4	8.7	168799	9	AC009531 Homo sapi
c 25	409	6.1	482	11	G36805 SHGC-54237
c 26	389.4	5.8	486	6	BD110970 EST and e
c 27	378.4	5.6	154865	9	AC099757 Homo sapi
c 28	378.4	5.6	163314	2	AL590557 Homo sapi
c 29	272	4.0	198463	9	AL353683 Human DNA
c 30	268.6	4.0	152695	2	AC142204 Homo sapi
c 31	268.6	4.0	205619	2	AC133567 Homo sapi
c 32	268.6	4.0	212166	2	AC142200 Homo sapi
c 33	266.8	4.0	3155	3	DWY16899 Drosophila

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

34 266.2 4.0 164076 9 AC008006 AC008006 Homo sapi
c 35 265.4 4.0 173275 9 AC092375 AC092375 Homo sapi
36 265 3.9 166628 2 AC145137 AC145137 Homo sapi
c 37 265 3.9 188076 2 AC023629 AC023629 Homo sapi
c 38 265 3.9 197752 2 AC145130 AC145130 Homo sapi
c 39 264 3.9 90906 9 AC079767 AC079767 Homo sapi
40 264 3.9 148012 2 AC138995 AC138995 Homo sapi
41 263.8 3.9 107037 9 HSJ678EE16 AL122004 Human DNA
c 42 263.4 3.9 114491 9 AC010331 AC010331 Homo sapi
c 43 263 3.9 170613 9 AC106788 AC106788 Homo sapi
44 263 3.9 202004 9 HUA001549 AF001549 Human Chr
c 45 262.4 3.9 167672 2 AC132806 AC132806 Homo sapi

Search completed: January 7, 2004, 17:54:50
Job time : 23479 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2004, 04:37:20 ; Search time 1564 Seconds
(without alignments)
11593.430 Million cell updates/sec

Title: US-10-082-272-1
Perfect score: 6717
Sequence: 1 gcgcgcgcgtcccccagccca.....taaaaaaaaaaaaaaaaaaa 6717

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 19Jun03: *
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT: *
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT: *
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT: *
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT: *
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT: *
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT: *
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT: *
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT: *
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT: *
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT: *

11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT: *
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT: *
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT: *
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT: *
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT: *
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT: *
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT: *
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT: *
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT: *
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT: *
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT: *
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT: *
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT: *
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT: *
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Description
No.	Score					
1	947	14.1	1082	24	ABS70452	Human bone remodel
2	841	12.5	1143	25	ABX70833	Novel human cDNA s
3	633.8	9.4	900	22	AA194043	Human neuroblastom
c	614.8	9.2	892	22	AA194044	Human neuroblastom
5	540.2	8.0	631	22	AAS34058	Human cDNA encodin
6	385.8	5.7	790	24	AAD42842	Human DNA #1 co-ex
7	268.4	4.0	2100	23	ABL17451	Drosophila melanog
c	263	3.9	31405	22	AAK67293	Human immune/haema
9	263	3.9	31405	22	AAK74865	Human immune/haema
10	263	3.9	31405	22	AAK83153	Human immune/haema
11	259.6	3.9	128600	24	ABK83461	Human cDNA differe
12	258.4	3.8	21332	22	AAK74878	Human immune/haema
13	258.4	3.8	21332	22	AAK83177	Human immune/haema
14	258.2	3.8	14258	22	AAK83210	Human immune/haema
15	258.2	3.8	14260	22	AAK83183	Human immune/haema
16	256.2	3.8	15810	24	AAS16995	Human atrionatriur
17	255.4	3.8	15364	22	AAK83152	Human immune/haema
c	253.2	3.8	32204	22	AAS39620	Geromic sequence #
c	253.2	3.8	32204	22	AAK89019	Human digestive sy
20	253.2	3.8	32204	22	AAK91533	Human digestive sy
21	253.2	3.8	32204	22	AA157790	Human colorectal c
22	253.2	3.8	32204	24	ABS99967	Genomic DNA #171 e
23	253	3.8	21621	22	AAK74867	Human immune/haema
24	251.8	3.7	14260	22	AAK83217	Human immune/haema
25	251.8	3.7	24102	22	AAK74877	Human immune/haema
26	251.4	3.7	3772	23	ABV23884	Human prostate exp
27	251.4	3.7	3772	23	ABV29765	Human prostate exp
c	250.8	3.7	3128	22	AAK71948	Human immune/haema
29	250.8	3.7	34831	22	AAK82518	Human immune/haema
30	250.4	3.7	2637	24	ABR88014	cDNA encoding huma
c	250.2	3.7	125439	24	ABQ88177	Human osteoblast d
32	250	3.7	15772	22	AAK83220	Human immune/haema

c 33 250 3.7 1503841 24 ABT00010 Human neuregulin 1
c 34 250 3.7 1503841 24 ABT01503 Human neuregulin 1
c 35 250 3.7 1503900 22 AAK95240 Human neuregulin-1
c 36 250 3.7 1503900 22 AAK96733 Human neuregulin-1
c 37 249.6 3.7 6547 22 AAK93105 Human immune/haema
38 249.6 3.7 6547 25 ABZ74497 Secreted protein 9
c 39 249.6 3.7 29695 24 ABO78853 Human PPM1G serine
c 40 249.6 3.7 27289 22 AAS34624 Human DNA for a no
c 41 249.2 3.7 121724 24 ABO88143 Human osteoblast d
c 42 249 3.7 18488 22 AAK93173 Human immune/haema
c 43 248.6 3.7 13774 22 AAK93209 Human immune/haema
c 44 248.6 3.7 174424 24 ABL68122 Ovary cancer relat
c 45 248.4 3.7 28123 24 ABS98441 Human multidrug re

Search completed: January 7, 2004, 11:23:28
Job time : 1581 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2004, 09:48:03 ; Search time 12380 Seconds
(without alignments)
13196.847 Million cell updates/sec

Title: US-10-082-272-1

Perfect score: 6717

Sequence: 1 gcgcgcgcgtccccacgcca.....taaaaaaaaaaaaaaaaaaaaaa 6717

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htci:*

9: gb_estli:*

10: gb_est2:*

11: gb_htci:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
c 1	1	1516.8	22.6	4026	11	AK052389	Mus muscu
c 2	2	798.2	11.9	3487	11	AK052155	Mus muscu
c 3	3	677	10.1	901	13	BQ216652	AGENCOURT
c 4	4	652.6	9.7	969	13	BX388215	BX388215
c 5	5	649.4	9.7	697	13	BX324356	BX324356
c 6	6	519.2	7.7	536	2	HSW096259	Homo sapi
c 7	7	472.2	7.0	477	9	AI936589	wid2906.x
c 8	8	468	7.0	552	2	HSW092075	Homo sapi
c 9	9	462.8	6.9	466	9	AA937310	On16H09.s
c 10	10	435.6	6.5	575	12	BM087995	501340 MA
c 11	11	425	6.3	425	9	AI808884	wf66a05.x
c 12	12	411	6.1	411	9	AA960800	on96h02.s
c 13	13	409	6.1	482	14	N93760	zb64c01.s1
c 14	14	393.2	5.9	641	10	BB652125	BB652125
c 15	15	385	5.7	649	14	CB441644	692147 MA
c 16	16	366	5.4	366	10	BE046007	hd91e03.x
c 17	17	353	5.3	384	9	AA700765	z166a02.s
c 18	18	343	5.1	549	12	BF109070	BP109070
c 19	19	341	5.1	456	14	R02483	ye86c03.r1
c 20	20	333.6	5.0	369	10	BE049094	xr72a06.x
c 21	21	333	5.0	333	9	AI207046	qf80c08.x
c 22	22	319	4.7	458	13	BY385297	BY385297
c 23	23	308.8	4.6	600	28	AQ681683	HS_2161_A
c 24	24	306.8	4.6	638	10	BB480212	BB480212
c 25	25	302.8	4.5	396	10	BB662398	BB662398
c 26	26	296	4.4	686	13	BU358229	603479159
c 27	27	255.2	3.8	667	10	BB659345	BB659345

C	28	250.8	3.7	544	10	BG739841
C	29	248.4	3.7	339	2	BSM070969
C	30	248.4	3.7	1374	11	BC017002
C	31	247.8	3.7	598	28	AQ489530
C	32	247.8	3.7	667	29	AG153670
C	33	247.4	3.7	663	2	BSM072801
C	34	246	3.7	605	14	CA434553
C	35	246	3.7	759	28	AQ386056
C	36	245.8	3.7	493	9	AU147922
C	37	245.4	3.7	582	28	AQ385524
C	38	244.8	3.6	625	12	BM989011
C	39	244.2	3.6	1043	12	BM919569
C	40	243.8	3.6	549	12	BM310229
C	41	243.2	3.6	488	28	AQ219156
C	42	243	3.6	489	28	B75932
C	43	243	3.6	790	29	AG185221
C	44	242.6	3.6	894	28	AQ787773
C	45	242.2	3.6	383	10	BG391274

Search completed: January 7, 2004, 21:22:33
Job time : 12398 secs

BG739841	602630570
Bx480803	Homo sapi
BC017002	Homo sapi
AQ489530	RPCI-11-2
AG153670	Pan trogl
Bx482633	Homo sapi
CA434553	UI-H-DH0-
AQ386056	RPCI11-14
AU147922	AU147922
AQ385524	RPCI11-14
BM989011	UI-H-DF0-
BM919569	AGENCOURT
BM310229	ih09f10.X
AQ219156	HS_3253_B
B75932	RPCI11-12NI
AG185221	Pan trogl
AQ787773	HS_3072_A
BG391274	60241731B